



IFWO

RAW SEQUENCE LISTING

DATE: 08/30/2004

PATENT APPLICATION: US/10/694,779

TIME: 12:56:10

Input Set : N:\Crf3\RULE60\10694779.raw

Output Set: N:\CRF4\08302004\J694779.raw

1 <110> APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
 2 <120> TITLE OF INVENTION: F0F1-ATPase polypeptides and their genes
 3 <130> FILE REFERENCE: 11329US1
 4 <140> CURRENT APPLICATION NUMBER: US/10/694,779
 5 <141> CURRENT FILING DATE: 2003-10-29
 6 <150> PRIOR APPLICATION NUMBER: US/09/901,884
 7 <151> PRIOR FILING DATE: 2001-07-09
 8 <150> PRIOR APPLICATION NUMBER: JP 2000-234317
 9 <151> PRIOR FILING DATE: 2000-08-02
 10 <160> NUMBER OF SEQ ID NOS: 21
 11 <170> SOFTWARE: PatentIn version 2.1
 13 <210> SEQ ID NO: 1
 14 <211> LENGTH: 304
 15 <212> TYPE: PRT
 16 <213> ORGANISM: Corynebacterium ammoniagenes
 17 <400> SEQUENCE: 1
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 19 1 5 10 15
 20 Ala Pro Tyr Asp Val Asp Asn Arg Thr Ala Arg Thr Arg Glu Arg Thr
 21 20 25 30
 22 Leu Ser Val Thr Thr Leu Ala Met Lys Gly Ser Phe His Ala Pro Glu
 23 35 40 45
 24 Leu Asp Pro Glu Phe Phe Pro Gly Gln Tyr Tyr Gly Asp Ile Leu Phe
 25 50 55 60
 26 Asp Asp Val Leu Gly Gly Trp Phe Ala Leu Asp Arg Ile Met Leu Val
 27 65 70 75 80
 28 Arg Leu Leu Met Thr Ala Val Leu Val Leu Leu Phe Ile Ala Ala Phe
 29 85 90 95
 30 Arg Asn Pro Lys Leu Val Pro Lys Gly Leu Gln Asn Val Ala Glu Tyr
 31 100 105 110
 32 Ala Leu Asp Phe Val Arg Ile His Ile Ala Glu Asp Ile Leu Gly Lys
 33 115 120 125
 34 Lys Glu Gly Arg Arg Phe Leu Pro Leu Leu Ala Ala Ile Phe Phe Gly
 35 130 135 140
 36 Thr Leu Phe Trp Asn Val Ser Thr Ile Ile Pro Ala Leu Asn Ile Ser
 37 145 150 155 160
 38 Ala Asn Ala Arg Ile Gly Met Pro Ile Val Leu Ala Gly Ala Ala Tyr
 39 165 170 175
 40 Ile Ala Met Ile Tyr Ala Gly Thr Lys Arg Tyr Gly Phe Gly Lys Tyr
 41 180 185 190
 42 Val Lys Ser Ser Leu Val Ile Pro Asn Leu Pro Pro Ala Leu His Leu
 43 195 200 205
 44 Leu Val Val Pro Ile Glu Phe Phe Ser Thr Phe Ile Leu Arg Pro Val

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45          210          215          220
46      Thr Leu Ala Ile Arg Leu Met Ala Asn Phe Leu Ala Gly His Ile Ile
47      225          230          235          240
48      Leu Val Leu Leu Tyr Ser Ala Thr Asn Phe Phe Phe Trp Gln Leu Asn
49          245          250          255
50      Gly Trp Thr Ala Met Ser Gly Val Thr Leu Leu Ala Ala Val Leu Phe
51          260          265          270
52      Thr Val Tyr Glu Ile Ile Ile Ile Phe Leu Gln Ala Tyr Ile Phe Ala
53          275          280          285
54      Leu Leu Thr Ala Val Tyr Ile Glu Leu Ser Leu His Ala Asp Ser His
55          290          295          300
57 <210> SEQ ID NO: 2
58 <211> LENGTH: 79
59 <212> TYPE: PRT
60 <213> ORGANISM: Corynebacterium ammoniagenes
61 <400> SEQUENCE: 2
62      Met Asn Asp Ile Ile Leu Ala Gln Ala Thr Glu Thr Ser Phe Asp Gly
63          1          5          10          15
64      Leu Gln Ser Ile Gly Tyr Gly Leu Ala Thr Ile Gly Pro Gly Leu Gly
65          20          25          30
66      Ile Gly Ile Leu Val Gly Lys Thr Val Glu Gly Met Ala Arg Gln Pro
67          35          40          45
68      Glu Met Ala Gly Gln Leu Arg Thr Thr Met Phe Leu Gly Ile Ala Phe
69          50          55          60
70      Val Glu Ala Leu Ala Leu Ile Gly Leu Val Ala Gly Phe Leu Phe
71          65          70          75
73 <210> SEQ ID NO: 3
74 <211> LENGTH: 189
75 <212> TYPE: PRT
76 <213> ORGANISM: Corynebacterium ammoniagenes
77 <400> SEQUENCE: 3
78      Met Asn Asn Val Phe Tyr Tyr Leu Ala Ala Glu Gly Glu Ser Leu Pro
79          1          5          10          15
80      Leu Glu Gly Gly Asn Ser Leu Leu Phe Pro Lys Ser Tyr Asp Ile Val
81          20          25          30
82      Trp Ser Leu Ile Pro Phe Leu Ile Ile Leu Ile Val Phe Ala Met Phe
83          35          40          45
84      Val Ile Pro Lys Phe Gln Glu Leu Leu Gln Glu Arg Glu Asp Arg Ile
85          50          55          60
86      Glu Gly Gly Ile Lys Arg Ala Glu Ala Gln Gln Ala Glu Ala Lys Ala
87          65          70          75          80
88      Ala Leu Glu Lys Tyr Asn Ala Gln Leu Ala Asp Ala Arg Ala Glu Ala
89          85          90          95
90      Ala Glu Ile Arg Glu Gln Ala Arg Glu Arg Gly Lys Gln Ile Glu Ala
91          100          105          110
92      Glu Ala Lys Thr Gln Ala Glu Glu Ala Arg Arg Ile Val Ala Gly
93          115          120          125
94      Gly Glu Lys Gln Leu Glu Ala Ser Arg Ala Gln Val Val Ala Glu Leu
95          130          135          140

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96      Arg Ser Asp Ile Gly Gln Asn Ser Ile Asn Leu Ala Glu Lys Leu Leu
97      145              150              155              160
98      Gly Gly Glu Leu Ser Glu Ser Thr Lys Gln Ser Ser Thr Ile Asp Asn
99              165              170              175
100     Phe Leu Ser Glu Leu Asp Ser Val Ala Ser Ala Gly Lys
101              180              185
103 <210> SEQ ID NO: 4
104 <211> LENGTH: 271
105 <212> TYPE: PRT
106 <213> ORGANISM: Corynebacterium ammoniagenes
107 <400> SEQUENCE: 4
108     Met Lys Ala Ala Ser Arg Glu Ser Leu Ala Ser Ala Thr Glu Ser Leu
109         1              5              10              15
110     Asp Ser Asn Leu Ala Ala Gln Ala Gly Val Ala Val Ser Thr Met Thr
111         20              25              30
112     Gly Met Glu Leu Phe Glu Val Ser Gln Val Leu Gly Asp Asp Arg Glu
113         35              40              45
114     Leu Arg Gly Ala Val Ile Asp Glu Ser Ala Ser Thr Glu Ser Arg Lys
115         50              55              60
116     Lys Leu Val Asn Asp Leu Phe Gly Ala Lys Val Ser Pro Ala Thr Leu
117         65              70              75              80
118     Gln Val Leu Glu Gln Ile Ala Ser Ser Lys Trp Ser Ser Ala Arg Glu
119         85              90              95
120     Met Val Ser Gly Leu Ile Ala Leu Ser Arg Arg Ala Leu Met Arg Gly
121         100             105             110
122     Ala Glu Ser Glu Gly Gln Leu Gly Gln Val Glu Asp Glu Leu Phe Arg
123         115             120             125
124     Leu Ser Arg Ile Leu Asp Arg Glu Gly Glu Leu Thr Gln Leu Leu Ser
125         130             135             140
126     Asp Arg Ala Ala Glu Pro Ala Arg Lys Arg Lys Leu Leu Ala Asp Val
127         145             150             155             160
128     Leu Tyr Gly Lys Val Thr Lys Phe Thr Glu Ala Leu Ala Leu Gln Val
129         165             170             175
130     Ile Asp Arg Pro Glu His Asn Pro Ile Asp Asp Ile Ala Asn Leu Ala
131         180             185             190
132     Ala Glu Ala Ala Gln Leu Gln Gly Arg Thr Val Ala His Val Val Ser
133         195             200             205
134     Ala Gly Glu Leu Asn Glu Gly Gln Gln Ala Val Leu Ala Glu Lys Leu
135         210             215             220
136     Gly Lys Ile Tyr Gly Arg Ala Met Ser Ile His Ser Glu Val Asp Thr
137         225             230             235             240
138     Ser Leu Leu Gly Gly Met Thr Ile Arg Val Gly Asp Glu Val Ile Asp
139         245             250             255
140     Gly Ser Thr Ala Gly Lys Ile Glu Arg Leu Arg Thr Ala Leu Lys
141         260             265             270
143 <210> SEQ ID NO: 5
144 <211> LENGTH: 546
145 <212> TYPE: PRT
146 <213> ORGANISM: Corynebacterium ammoniagenes

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147 <400> SEQUENCE: 5

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148 Met Ala Glu Leu Thr Ile Ser Ser Asp Glu Ile Arg Ser Ala Ile Ala
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150 Asn Tyr Thr Ser Ser Tyr Ser Ala Glu Ala Ser Arg Glu Glu Val Gly
151 20 25 30
152 Val Val Ile Ser Ala Ala Asp Gly Ile Ala Gln Val Ser Gly Leu Pro
153 35 40 45
154 Ser Val Met Ala Asn Glu Leu Leu Glu Phe Pro Gly Gly Val Ile Gly
155 50 55 60
156 Val Ala Gln Asn Leu Glu Thr Asn Ser Ile Gly Val Val Ile Leu Gly
157 65 70 75 80
158 Asn Tyr Glu Ser Leu Lys Glu Gly Asp Gln Val Lys Arg Thr Gly Glu
159 85 90 95
160 Val Leu Ser Ile Pro Val Gly Glu Glu Phe Leu Gly Arg Val Ile Asn
161 100 105 110
162 Pro Leu Gly Gln Ala Ile Asp Gly Leu Gly Pro Ile Ala Gly Glu Glu
163 115 120 125
164 Asp Arg Val Leu Glu Leu Gln Ala Pro Ser Val Leu Gln Arg Gln Pro
165 130 135 140
166 Val Glu Glu Pro Met Gln Thr Gly Ile Lys Ala Ile Asp Ala Met Thr
167 145 150 155 160
168 Pro Ile Gly Arg Gly Gln Arg Gln Leu Ile Ile Gly Asp Arg Lys Thr
169 165 170 175
170 Gly Lys Thr Ala Val Cys Ile Asp Thr Ile Leu Asn Gln Lys Ala Asn
171 180 185 190
172 Trp Glu Ser Gly Asp Lys Asn Lys Gln Val Arg Cys Ile Tyr Val Ala
173 195 200 205
174 Ile Gly Gln Lys Gly Ser Thr Ile Ala Gly Val Arg Lys Thr Leu Glu
175 210 215 220
176 Glu Gln Gly Ala Leu Glu Tyr Thr Thr Ile Val Ala Ala Pro Ala Ser
177 225 230 235 240
178 Asp Ser Ala Gly Phe Lys Trp Leu Ala Pro Phe Ser Gly Ala Ala Leu
179 245 250 255
180 Gly Gln His Trp Met Tyr Gln Gly Asn His Val Leu Val Ile Tyr Asp
181 260 265 270
182 Asp Leu Thr Lys Gln Ala Glu Ala Tyr Arg Ala Ile Ser Leu Leu Leu
183 275 280 285
184 Arg Arg Pro Pro Gly Arg Glu Ala Tyr Pro Gly Asp Val Phe Tyr Leu
185 290 295 300
186 His Ser Arg Leu Leu Glu Arg Ala Ala Lys Leu Ser Asp Asp Leu Gly
187 305 310 315 320
188 Ala Gly Ser Leu Thr Ala Leu Pro Ile Ile Glu Thr Lys Ala Asn Asp
189 325 330 335
190 Val Ser Ala Phe Ile Pro Thr Asn Val Ile Ser Ile Thr Asp Gly Gln
191 340 345 350
192 Val Phe Leu Glu Ser Asp Leu Phe Asn Gln Gly Val Arg Pro Ala Ile
193 355 360 365
194 Asn Val Gly Val Ser Val Ser Arg Val Gly Gly Ala Ala Gln Thr Lys
195 370 375 380

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196 Gly Met Lys Lys Val Ala Gly Asn Leu Arg Leu Asp Leu Ala Ser Tyr
197 385 390 395 400
198 Arg Asp Leu Gln Gly Phe Ala Ala Phe Ala Ser Asp Leu Asp Pro Val
199 405 410 415
200 Ser Lys Ala Gln Leu Glu Arg Gly Glu Arg Leu Val Glu Ile Leu Lys
201 420 425 430
202 Gln Ser Glu Ser Ser Pro Gln Ala Val Glu Tyr Gln Met Val Ser Ile
203 435 440 445
204 Phe Leu Ala Glu Glu Gly Val Phe Asp Val Val Pro Val Glu Asp Val
205 450 455 460
206 Arg Arg Phe Glu Ala Asp Val Gln Glu Tyr Leu Gln Gln Asn Thr Pro
207 465 470 475 480
208 Glu Val Tyr Glu Gln Ile Ala Gly Gly Lys Ala Phe Thr Asp Glu Ser
209 485 490 495
210 Lys Glu Ala Leu Leu Ala Ala Ala Lys Asp Phe Thr Pro Ser Phe Arg
211 500 505 510
212 Thr Thr Glu Gly His Asn Leu Gly Thr Glu Ala Pro Val Asp Pro Leu
213 515 520 525
214 Ala Glu Glu Glu Val Lys Lys Thr Glu Val Thr Val Ser Arg Lys Ser
215 530 535 540
216 Ala Lys
217 545
219 <210> SEQ ID NO: 6
220 <211> LENGTH: 327
221 <212> TYPE: PRT
222 <213> ORGANISM: Corynebacterium ammoniagenes
223 <400> SEQUENCE: 6
224 Met Ala Asn Leu Arg Glu Leu Arg Asp Arg Ile Arg Ser Val Asn Ser
225 1 5 10 15
226 Thr Lys Lys Ile Thr Lys Ala Gln Glu Leu Ile Ala Thr Ser Arg Ile
227 20 25 30
228 Thr Lys Ala Gln Ala Lys Val Asp Ala Ala Ala Pro Tyr Ala His Glu
229 35 40 45
230 Met Ser Asn Met Met Asp Arg Leu Ala Ser Ala Ser Ser Leu Glu His
231 50 55 60
232 Pro Met Leu Arg His Arg Glu Asn Gly Lys Val Ala Ala Val Leu Val
233 65 70 75 80
234 Val Ser Ser Asp Arg Gly Met Cys Gly Gly Tyr Asn Asn Asn Val Phe
235 85 90 95
236 Lys Lys Ala Ala Glu Leu Glu Gly Leu Leu Arg Gly Gln Gly Phe Asp
237 100 105 110
238 Val Val Arg Tyr Val Thr Gly Ser Lys Gly Val Gly Tyr Tyr Asn Phe
239 115 120 125
240 Arg Glu Lys Glu Val Val Gly Ala Trp Thr Gly Phe Ser Gln Asp Pro
241 130 135 140
242 Ser Trp Glu Gly Thr His Asp Val Arg His His Leu Val Asp Gly Phe
243 145 150 155 160
244 Ile Ala Gly Ser Glu Gly Thr Thr Pro Ala Arg Gln Gly Val Asn Thr
245 165 170 175

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VERIFICATION SUMMARY

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TIME: 12:56:11

Input Set : N:\Crf3\RULE60\10694779.raw

Output Set: N:\CRF4\08302004\J694779.raw

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L:572 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:21
L:574 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:21
L:576 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:21
L:578 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:21
L:580 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:21
L:582 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:21